

Table S1. GO categories enriched among *L. major* genes in common and specific to human and mouse infections.

GO ID	GO term	Number DE Genes	Category Size	P Value
Upregulated, human and mouse				
GO:0051920	peroxiredoxin activity	7	8	3.93E-08
GO:0016209	antioxidant activity	7	9	1.51E-07
Downregulated, human and mouse				
GO:0005516	calmodulin binding	11	11	0.00E+00
GO:0004674	protein serine/threonine kinase activity	52	198	9.30E-14
GO:0004672	protein kinase activity	52	204	3.53E-13
GO:0006468	protein phosphorylation	52	208	8.03E-13
GO:0004713	protein tyrosine kinase activity	46	170	8.85E-13
GO:0009434	motile cilium	11	12	2.91E-11
GO:0009190	cyclic nucleotide biosynthetic process	9	12	1.45E-07
GO:0016849	phosphorus-oxygen lyase activity	9	12	1.45E-07
GO:0005524	ATP binding	93	679	2.35E-06
GO:0003777	microtubule motor activity	21	78	2.36E-06
GO:0035556	intracellular signal transduction	10	20	4.01E-06
GO:0006633	fatty acid biosynthetic process	10	26	3.51E-05
GO:0030286	dynein complex	7	14	8.08E-05
Upregulated, human only				
GO:0000786	nucleosome	20	30	1.05E-11
GO:0006334	nucleosome assembly	21	33	1.06E-11
GO:0046982	protein heterodimerization activity	20	31	2.51E-11
GO:0006412	translation	61	224	4.72E-09
GO:0015986	ATP synthesis coupled proton transport	16	27	2.40E-08
GO:0003735	structural constituent of ribosome	51	180	3.02E-08
GO:0005840	ribosome	49	173	5.89E-08
GO:0015991	ATP hydrolysis coupled proton transport	13	23	1.28E-06
GO:0008234	cysteine-type peptidase activity	9	13	3.73E-06
GO:0046933	proton-transporting ATP synthase activity	7	10	7.18E-05
GO:0006886	intracellular protein transport	23	76	9.44E-05
GO:0030117	membrane coat	9	17	1.07E-04
GO:0015031	protein transport	16	49	3.08E-04
GO:0046034	ATP metabolic process	4	4	3.40E-04
GO:0033180	proton-transporting V-type ATPase	4	4	3.70E-04
GO:0016192	vesicle-mediated transport	16	50	4.46E-04
GO:0015078	hydrogen ion transmembrane transporter activity	7	13	5.29E-04
Downregulated, human only				
GO:0007018	microtubule-based movement	22	101	4.70E-05
GO:0006310	DNA recombination	6	10	6.58E-05
Upregulated, mouse only				
GO:0006950	response to stress	17	23	1.47E-12
GO:0006486	protein glycosylation	8	13	1.09E-05
GO:0008378	galactosyltransferase activity	6	8	3.21E-05
GO:0007155	cell adhesion	5	6	6.70E-05
GO:0008160	protein tyrosine phosphatase activator activity	4	4	1.15E-04
GO:0042025	host cell nucleus	4	4	1.15E-04
GO:0044081	modulation by symbiont of host nitric oxide-mediated signal transduction	4	4	1.15E-04
GO:0075130	modulation by symbiont of host protein kinase-mediated signal transduction	4	4	1.15E-04
GO:0006260	DNA replication	13	39	1.35E-04
GO:0051082	unfolded protein binding	18	68	2.00E-04
Downregulated, mouse only				
GO:0006412	translation	71	224	2.04E-18
GO:0005840	ribosome	61	173	2.06E-18
GO:0003735	structural constituent of ribosome	62	180	3.53E-18
GO:0005622	intracellular	78	379	3.15E-09
GO:0006184	GTP catabolic process	17	55	3.43E-05
GO:0005779	integral component of peroxisomal membrane	5	6	7.39E-05
GO:0016559	peroxisome fission	5	6	7.39E-05
GO:0008234	cysteine-type peptidase activity	7	13	1.37E-04

Table S1: Enriched GO categories among *L. major* genes in common and specific to human and mouse infections. GOseq was used to identify GO categories enriched among DE genes during the metacyclic promastigote to 4 hpi intracellular transition. Genes that were expressed in the same direction in human and mouse host systems, those specific to infection in the human system, and those specific to infection in the mouse system were evaluated with up- and down-regulated genes considered separately (P value < 0.05).